

## CLAIMS

1. A protease variant comprising:

a) an insertion, substitution or deletion of one of the amino acid residues

5 K,H,R,E,D,Q,N,C,V,L,I,P,M,F,W,Y,G,A,S,T in one or more of the positions 62, 68, 97, 98, 99, 106, 131, 170, 245, 252,

in combination with at least one of the following modifications

\*0AQSVPWG; A1T,V; Q2L; S3T,A,L; V4L,A; I8V,T; S9G,D,R,K,L,V; R10H,K; V11A; Q12D; A13V; P14S,T,D,A,M,V,K,Q,L,H,R,I; A15M,T; A16P; H17R; N18S,H; R19W,K,L,F,G,I; 10 G20\*,R,A; L21F,LP,LW,LA,LG; T22S,A,K,TV,TG,TL,TW,TV,G,L,TY; G23S; S24P; K27R, V28I; V30I; I35T,V;T38S; P40L; N43D; R45H,K; G46D; A48T; S49N; F50S; V51A,I,D; P52V,A; P55S,A; S57P; G61E,D,S,R,GP; N62D,ND,NE,DE,NG,E,S; V68A,S,L,I; T71A; I72V; L75I; N76S,D; N77S; S78T; V81A; A85T; S87C; A88V,T; E89G; K94N; V95C,T; L96LA,LG; G97E,D,W,A,GG,GA,GV,N,GS; A98S,D,E,T,AS,AD,AV,AE,AH,Q,N,M,L,G,R,V,S;

15 S99D,L,A,AD,SD,SM,SG,DA,P,G,N,C,M,V,I; G100S,GE,C; S101SA, SK; G102D,S; S103D,E,Y,L,Q,H,T; V104T,S,R,I,N,M,L,D; S106D,E,T,M,G,A,L,F,I; I107T,V,M; A108V,T,S; L111I,V; A114V; N116S,D; G118D; M119L,I,V,A,S; H120N,D,Q,K,E,Y,S; V121A; L124C; L126I; G127E; S128N,I,G,C; P129PSN,T,E,D,S,N,A; S130P,T,C,\*; P131M,F,W,L,A,H,T,\*,PA,S,Q,R,E,G,D,C; S132G,T; A133ASA; T134A; Q137H,E,D; A138G,V; 20 V139L,I; N140D, K; T143A; S144D, N,P; R145G; V150I; A151V,G; A152P; A158T,V,C,E,L,D, M; G160A,D; S163G,C,N,A; Y167K,A,I; A168G; A169G; R170C,S,H,L; Y171C; A172V; N173D; A174V; M175L,I,V,A,S,T; N183D; N184D,S; N185S,D; R186L,C,H; S188G; S190A; Y192H; G195F,E; V203S,A,L,Q,M, F,I; N204T,D,S; Q206L; Y209C,H; G211D; S212N,L; T213A; Y214C,H; A215D,T; N218D,S; M222L,I,V,A,S; A223G; T224A,S; A228T; A230V; A232S,L,T,P; 25 V234I; Q236A,L,D,T,C,M,F,S; K237R; N238D; P239T,S; S240F; S242T; V244I,M,A; Q245R,K,E,D,T,F,N,V,W,G,I,S,C,L,A,M; N248P,D,S; K251E,R; N252G,H,D,V,M,S,T,E,Y,S,Q,K,A,L; A254S; T255A,S; S256N,R,G; L257G; G258K, S259A,N,G; T260A,R; N261D; L262S, Q,V; Y263H,F; G264E; S265G,R,N; V268L,I; N269T; N296K; E271A; T274S,L,A,R, or

30 b) one of the following combination variants

A108T+L111V; L124I+S125A; P129S+S130AT; L96LA+A151G+V203A; S49N+V203L+N218D; S3T+A16P+R45C+G100S+A230V; I8V+R19K+V139I; N76D+A174AL+A194P+A230V; N185R; N62NE; H120Q+Q137E, G61GE, G61GS, G100L, A133D, V68A, N123D, L111F+Y263H, V11A+G61GE+V227A+S240F, A133E+S144K+N218D, S128A+P129S+S130SP,

S9R+A15T+T22TQ+S101P, S9R+A15T+H120R+Q137D+N173S, G97E, Q245W,  
 S9R+A15T+L96LG+Q137E+Y209H, S9R+A15T+L111V+Q137E+G211D,  
 S9R+A15T+L111I+Q137E, S9R+A15T+L111I+H120N+Q137E,  
 S9R+A15T+L96LG+H120Q+Q137E, S9R+A15T+T260M, S9R+A15T, Q245I,  
 5 S9R+A15T+H120G+Q137E+N218D, S9R+A15T+S130P, Q245F, S9R+A15T+N218D,  
 G63E+N76D+A194P+A230V, S9R+A15T+T224A, G100S, S9R+A15T+D60DG,  
 A138V+V139I+A194P+N218D+A230V, A108V+A169G+R170A+Y171H,  
 I8V+P14L+R19L+V30I+I35V+S57P+P129S+Q137D+S144D+S256N, A133D+T134S+Q137A,  
 Q137D, A98AH, V51D, Q12E+P14L+A15T, G63E+N76D+A194P+A230V, Q12E+P14L+A15T,  
 10 G97GS, V51A+S163T; V139I+A151G; S9R+A15T+L96LG+S130\*; A169G+R170H or

c) one or more modifications in position 68, wherein said modification(s) comprise(s):  
 deletion, insertion and/or substitution of an amino acid residue selected from the group  
 consisting of K,H,R,E,D,Q,N,C,V,L,I,P,M,F,W,Y,G,A,S and T.

15 2. A protease variant of claim 1 comprising the combination of one or more of the  
 modifications

X62D,E,S,XD,XE,XG,DE

X68A,S,L,I

X97E,D,W,A,N,XG,XA,XV,XS

20 X98S,D,E,T,N,M,L,G,R,V,XS,XD,XV

X99D,L,A,P,G,N,C,M,V,I,AD,XD,XM,XG,DA

X106D,E,T,M,G,A,L,F,I

X131M,F,W,L,A,H,T,\*,S,Q,R,E,G,D,C,XA

X170C,S,H,L

25 X245R,K,E,D,T,F,N,V,W,G,I,S,C,L,A,M

X252G,H,D,V,M,S,T,E,Y,S,Q,K,A,L

with at least one of the following modifications

\*0AQSVPWG; A1T,V; Q2L; S3T,A,L; V4L,A; I8V,T; S9G,D,R,K,L,V; R10H,K; V11A; Q12D;  
 A13V; P14S,T,D,A,M,V,K,Q,L,H,R,I; A15M,T; A16P; H17R; N18S,H; R19W,K,L,F,G,I;  
 30 G20\*,R,A; L21F,LP,LW,LA,LG; T22S,A,K,TV,TG,TL,TW,TV,G,L,TY; G23S; S24P; K27R, V28I;  
 V30I; I35T,V;T38S; P40L; N43D; R45H,K; G46D; A48T; S49N; F50S; V51A,I,D; P52V,A;  
 P55S,A; S57P; G61E,D,S,R,GP; N62D,ND,NE,DE,NG,E,S; V68A,S,L,I; T71A; I72V; L75I;  
 N76S,D; N77S; S78T; V81A; A85T; S87C; A88V,T; E89G; K94N; V95C,T; L96LA,LG;  
 G97E,D,W,A,GG,GA,GV,N,GS; A98S,D,E,T,AS,AD,AV,AE,AH,Q,N,M,L,G,R,V,S;

S99D,L,A,AD,SD,SM,SG,DA,P,G,N,C,M,V,I; G100S,GE,C; S101SA, SK; G102D,S;  
S103D,E,Y,L,Q,H,T; V104T,S,R,I,N,M,L,D; S106D,E,T,M,G,A,L,F,I; I107T,V,M; A108V,T,S;  
L111I,V; A114V; N116S,D; G118D; M119L,I,V,A,S; H120N,D,Q,K,E,Y,S; V121A; L124C; L126I;  
G127E; S128N,I,G,C; P129PSN,T,E,D,S,N,A; S130P,T,C,\*;  
5 P131M,F,W,L,A,H,T,\*,PA,S,Q,R,E,G,D,C; S132G,T; A133ASA; T134A; Q137H,E,D; A138G,V;  
V139L,I; N140D, K; T143A; S144D, N,P; R145G; V150I; A151V,G; A152P; A158T,V,C,E,L,D,  
M; G160A,D; S163G,C,N,A; Y167K,A,I; A168G; A169G; R170C,S,H,L; Y171C; A172V; N173D;  
A174V; M175L,I,V,A,S,T; N183D; N184D,S; N185S,D; R186L,C,H; S188G; S190A; Y192H;  
G195F,E; V203S,A,L,Q,M, F,I; N204T,D,S; Q206L; Y209C,H; G211D; S212N,L; T213A;  
10 Y214C,H; A215D,T; N218D,S; M222L,I,V,A,S; A223G; T224A,S; A228T; A230V; A232S,L,T,P;  
V234I; Q236A,L,D,T,C,M,F,S; K237R; N238D; P239T,S; S240F; S242T; V244I,M,A;  
Q245R,K,E,D,T,F,N,V,W,G,I,S,C,L,A,M; N248P,D,S; K251E,R;  
N252G,H,D,V,M,S,T,E,Y,S,Q,K,A,L; A254S; T255A,S; S256N,R,G; L257G; G258K,  
S259A,N,G; T260A,R; N261D; L262S, Q,V; Y263H,F; G264E; S265G,R,N; V268L,I; N269T;  
15 N296K; E271A; T274S,L,A,R.

3. The protease variant of claim 1, comprising one or more of the following alterations:

G97E+A98S	V28I+A98AD+T224S
G97D+A98D	S99AD+M175V+P131F
V95C+G97W+A98E	S99AD+P131L
V95T+G97A+A98D	S9R+S99AD+P131W
S103Y+V104M+S106D	V68A+N116S+V139L+Q245R
V104T+S106D	S3T+A16P+R45C+G100S+A230V
S3T+A16P+S99SD+S144D+A158T+ A230V+T260R	I8V+S9R+A15T+R19W+V30I+G61D+ S99SD+S256N
S103D+V104T+S106T	V30I+S99SD+S256R
S103D+V104L+S106M	G61S+S99SD+V244I
S103D+V104T+S106G	V68A+V139L+S163G+N185S
S103D+V104S+S106A	S99SD+Y263H

S103H+V104N+S106D	V104N+S106T
S103E+V104I+S106T	S99SG+S144D
S103Q+V104T+S106E	V30I+S99SD
S103E+S106T	N18H+S99SD
S103E+V104R+S106A	S9R+T22S+S99SD+K251E
A108T+L111V	A48T+V68A+P131M
L124I+S125A	A15M+S99SM+V139I+V244I
L124C+P131*	P14T+A15M+S99SD
P129S+S130AT	I8V+S99SD+S144D+A228T
L96LA+A151G+V203A	I8V+R19K+V139I
S99SD+A108V+V139L	I35T+N62D
S99SD+S190A	N62D+S265G
S99SD+V203A	Q2L+N62D
S99SD+V139I	N62D+N76D
S99SD+A108V	R45H+G61E+V68A
S99SD+S106A+A151G	N62D+V121A
V68A+S106A	N62D+A215D
V68A+N185D+V203S	N62D+N238D
V68A+V139L	N62D+R145G
V68A+V139I	V4L+N62D+E89G
V68A+A158V	N62D+S188G+K251R
V68A+V203A	S49N+N62D
V68A+V203S	N62NE
V68A+V203L+S259A	V11A+N62DE

V68A+S106L	N62ND+N184S+S256G
V30I+V68A+V203S	N18S+N62D+I107T+A254S
V51A+V68A+S106T+A168G	S57P+N62ND
V51A+V68A+S106T+A168G	N62NE+V234I
V68A+N76S+V203M+P239T	Q137H+R170C+G195E
V68A+V203L	S99A+S101SA
V68A+L75I+V203Q	R10K+P14A+R19K+A98AS+S128N
V68A+T71A+V139L	T22A+R45K+A98AS+S128N
Y192H+V68A	A98AV+S99D+Y167K
V68A+S106A+A108T	S9G+P14K+Y167A+R170S
V68A+S106T+A108T	S9D+P14T+Y167A+R170S
V68S+A108S	S9R+P14M+A98AD
V68A+N76S+G211D	S9R+R19L+A98AD+E271A
V68A+S106T+A108T	S9R+P14S+R19F+A98AD
A151V+R170C	S99DA+P129PSN+P131A
P14D+A98AS+H120D+G195F+ S212N+M222S	S99AD+V244M+Q245K+N248D+ K251R+T255A+S256N
S49N+V203L+N218D	S9R+P14V+R19G+A98AD
V68A+S106M+N184D	S99AD+N248P+T255A+S256G
P55S+V68L+A158E+G160A	*0AQSVPWG+A98AD
V68A+A158C	T22A+S99AD
V68A+A158L+Y214C	K94N+A98T+S99L
A88V+S99AD+P131F	N76D+A174AL+A194P+A230V
P14T+A16P+I72V+S99SD+V244I+T260A	P40L+N218D+A232S+Q236L+Q245E+S259N
S99AD+P131F	A232L+Q236D+Q245E

R10H+N62D	A232T+Q236L+Q245D
V28I+A98AD+T224S	R170H+Q236A+Q245R
S9K+T22K+S99AD	A232L+Q236T+Q245D
P14S+S99AD+P131W	G97GG+P131H+Q137E+V268L
V68A+I72V+P131F	A88V+G97GV+P131H
S9R+S99AD	G97GA+H120Q+S130P+G264E
S9K+S99AD	G97GG+V139L
V28I+A88V+G100S+P131M	G97GG+Q137D
S103L+V104S+S106G	G97GG+H120D+Q137H
V68A+T224A	N185R
V68A+P131F	P131H+Q137E
A48T+V68A+P131M	V104I+H120N+P131H+Q137E
V68A+I72V+P131F	H120Q+Q137E
G100GE+P131F	S9R+A15T+G97GV+H120D
S99AD+P131F+T260A	G100S+H120Q+Q137H
R19G+A98AS	V68A+H120K+Q137E
G61R+N62D	G97GA+H120E
V68A+S106M+N184D	H120D+S128I+Q137D
P55S+V68L+A158E+G160A	G97GG+P131H
V68A+A158C	G97GG+H120N+L126I
R19W+G61S+S99SD+N204T+Y263H+ S265R	S9R+A15T+G97GA+H120D+P131H+ Q137E
A232T+Q236C	S9R+A15T+G97GV+P131T+Q137H
N62D+A232T+Q236C	S9R+A15T+G20*+L21F+N62D+Q245N
A232P+Q236L+Q245E	S9L+A15T+T22TV+V139L+Q245F

A232S+Q236L+Q245T+K251E	S132G+Q245F
S163C+Q236M+Q245T+S256G	S9R+A15T+T22TG+N62D+V139L+Q245V
N218D+A232L+Q236F+Q245F	S9L+A15T+T22TV+V139L+Q245F+L262S
S163N+A232L+Q236S+Q245E	S9R+A15T+T22TL+N62D+Q245W
A232S+Q236S+Q245E	V68A+A158L+Y214C
V68A+V203L	N62D+V150I
V68S+A158D	S3T+P14Q+A15M+R19K+N62D+S144D
I8V+A15T+R19K+A85T+S99SD+A114V+ V244I+S256N+Y263H	P14Q+R19W+V51I+G61E+S99SD+ V139I+T260R
L111F+Y263H	S3T+P14L+H17R+S99SD+V139I+S144D
P52V+S78T+S99SD	S3A+V30I+S99SD+S106G+N248S
A15M+S99SD+V268I	I8V+A15T+S99SD
S99G+S128N+N183D+A232L+Q236T+ Q245R	S3T+S9R+P14H+A15M+R19L+S99SD+ V139I
S99R+S101SA	S9R+A15T+G97GG+H120D+Q137E
L96LA+A98T+P131AA	S9R+A15T+G20A+G97GV+H120D+P131H
A98E+S99P	S163N+A232L+Q236A+Q245G
V28I+S99AD+P131F	N173D+A232L+Q236A+Q245N
S9R+A15T+G97GV+Q137H	P55S+V68A+S106M+A108T+P129T
V81A+P131T+A133S+Q137E	K27R+V68L+G118D+A158E
N43D+V68A+S106F+N238D	A98E+S99A+S101SK
V68A+V203F	V68A+N140D+T143A+S144N
V68A+S106E	N62D+N140K+T143A+S144D
V68A+S106I	S9F+P14T+R19L+A98AD
V68A+A158M+R170C	S9V+P14R+R19F+A98AD

V68A+P129T+N218D	S99A+S99SD+G258K+L262Q
V68S+P129E	S87C+S99SA+S99D+P131A
V68S+P129D	S99A+S99SD+G258K+L262Q
V68L+P129E+N261D	V28I+S99A+*99aD+P131F
G97GV+H120D	A85T+G102D+S106T+K237R
P131A+A133ASA	V68A+T71A
L111F+Y263H	G61GS
V11A+G61GE+V227A+S240F	G100L
A133E+S144K+N218D	A133D
S128A+P129S+S130SP	V68A
G61GE	N123D
S9R+A15T+T22TW+N204D+Q245I	Q245W+N252V
S9R+A15T+G97GG+P131S+Q137H	R45H+Y171C+Q245W+N252S
S9R+A15T+T22TG+N62D+V139L+Q245G	G20R+A48T+R170C+Q245W+N252Q
S9R+A15T+T22TL+N62D+I107V+V139L+Q245W	S9R+A15T+A16P+G97GA+P131S+Q137D+N204S
S9G+A15T+G97GA+Q137H	N218D+Q245W+N252E
S9R+A15T+V68A+Q245R	G20R+R170C+Q245R+N252V
S9R+A15T+G97GA+H120N+S212L	S9R+P14I+R19K+A98AD+T274S
S9R+A15T+L96LG+H120D+P131H+R186L	A98AE+V203I
S9R+A15T+G97GA+H120D+Q137D	V51A+V68A+S163G+V203A
N62D+N252T	N62D+Q245W+N252H
V4A+S9R+A15T+G97GV+H120D	N62D+Q245W+N252A
S9R+A15T+G97GV+H120D+Q137H	G20R+N62D+V244I+Q245W+N252E
S9R+A15T+L96LG+H120N+P131H+Q137E	N204D+Q245S



S9R+A15T+L96LG+H120D+P131S+Q137E	N62D+Q245W+N252E
S9R+A15T+H120N+P131T+N218D	N62D+Q245R+N252V
S9R+A15T+L21LP+T22TV+M119I+N218D+Q245I	S9R+A15T+S24P+G61E+A85T+P239S+Q245A
S9R+A15T+L96LG+H120D+G160D	G102S+M222S+Q245L+N252D
V68A+S106A+G118D+Q245R+T255S+L257G+T274L	A15M+V30I+N62D+S99N+L111I+V244A+S265N
S9R+A15T+G61E+A85T+P239L+Q245C	S9R+A15T+T22TG+N62D+V139L+Q245S
S9R+A15T+P131H+S144P	S3T+Q12D+R19W+V30I+S106G+I107M
S9R+A15T+G97GA+Q137E	V68A+A88T+V139L
S9R+A15T+G97GA+H120Q+P131H+Q137E	V51I+L111I+G118D+Q245R
S9R+A15T+L21LW+G100S+V139L+Q245V	V68A+V203L
S9R+A15T+G97GA+Q137H+N218S	A1T+V68A+N116D+G118D
S9R+A15T+L96LG+H120N+P131S+Q137H	V68A+G118D+Q245R
S9R+A15T+G97GA+H120N+Q137E	N62D+V139I+N183D+N185S+V203I+Q245R+L262S
S9R+A15T+L96LG+P131T+Q137H	N62D+I72V
S9R+A15T+L96LG+H120N+P131S	N62D+V81A+Q245R
S9R+A15T+V68A+Q137D	T22A+V68A+S106T+G118D
S9R+A15T+G97GA+H120Y+Q137H	V68A+L111I+V203I
S9R+A15T+G97GA+Q137D	G61E+V68A+A169G
S9R+A15T+K94N+H120N+P131H	V68A+L111V
S9R+A15T+L96LG+P131H+Q137D	V68A+G118D+V203A+K251R
S9R+A15T+F50S+H120D+P131H	V68A+G118D
S9R+A15T+G97GA+H120N+Q137D+N248D	A1V+V51A+V68A+V203I
S9R+A15T+L96LG+P131Q+Q137D	V68A+V139L+A223G

S9R+A15T+T22G+V139L+Q245L	N62D+Y214H+K237R
V139L+Q245R	V68A+S106A+G118D+Q245R
S9R+A15T+Q245F	S9R+A15T+T22A+N62D
S9R+A15T+Q245S	A98Q+S99D
S9R+A15T+G97GV+H120Q	S9R+P14I+R19K+A98AD
S9R+A15T+G97GA+Q137E+L262V	S9R+A15M+A16P+T22S+S99AD
S9R+A15T+G127E+P131R+Q137H	S99AD+T255R+S256N
S9R+A13V+A15T+I35V+N62D+Q245F	S9R+A15T+T22TQ+S101P
S9R+A15T+Q245V	S9R+A15T+H120R+Q137D+N173S
V139L+Q245F	G97E
S9R+A15T+T22A+V139L+Q245E	Q245W
S9R+A15T+T22L+V139L+Q245V+A254S	S9R+A15T+L96LG+Q137E+Y209H
S9R+R19L+A98AD	S9R+A15T+L111V+Q137E+G211D
P14R+A98AD	S9R+A15T+L111I+Q137E
S9R+A15T+Q245L	S9R+A15T+L111I+H120N+Q137E
S9R+A15T+G61E+A85T+P239S+Q245V	S9R+A15T+L96LG+H120Q+Q137E
S9R+A15T+G61E+A85T+Q206L+Q245R	S9R+A15T+T260M
P239T+Q245R	S9R+A15T
S9R+A15T+N62NG+Q245T	Q245I
S9R+A15T+G61GP+Q245L	S9R+A15T+H120G+Q137E+N218D
S9R+A15T+G61E+A85T+Q137H+Y209C+Q245G	I8V+P14L+R19L+V30I+I35V+S57P+P129S+Q137D+S144D+S256N
S9R+A15T+G61E+A85T+P239S+Q245C	Q245F
V68I+A98AD	S9R+A15T+N218D
V68A+N269K	G63E+N76D+A194P+A230V

N62D+Q245A+N252G+S265G	S9R+A15T+T224A
N218D+Q245G+N252H	G100S
S9R+A15T+G102S+M175T+Q245R+N252D	S9R+A15T+D60DG
S9R+A15T+N62D+Q245W+N252V	A138V+V139I+A194P+N218D+A230V
S9R+A15T+N62D+Q245R+N252M	A108V+A169G+R170A+Y171H
S9R+A15T+N62D+Q245W+N252S	S9R+A15T+S130P
S99SD+N204S+Q245R	A133D+T134S+Q137A
N62D+Q245R	Q137D
N62D+A151G	A98AH
V68A+S106T	V51D
S99A+S99SD+V203L	Q12E+P14L+A15T
A98AD+A215T	G63E+N76D+A194P+A230V
N62D+Q245G+N252T	Q12E+P14L+A15T
A152P+Q245R+N252T	G97GS
S163N+T213A+Q245R	Q245W+N252Y
S106L+Q245R+N252E	A169G+R170H
S9V+P14R+R19F+A98AD	Q12E+P14L+A15T
S9R+A15T+L111I+Q137E	P14R+A98AD
S9R+A15T+G97GA+Q137E	G100S
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S9R+A15T+G97GV+P131S	V68A+S106T

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S9R+A15T+F50S+H120D+P131H	S3L+N62D+S163A+S190A
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Q245I	Q245R+L262S
S9R+A15T+V68A+Q245R	V68A+S106A+G118D+Q245R
S9R+A15T+T22A+V139L+Q245E	V51I+L111I+G118D+Q245R
V139L+Q245R	N62D+Q245R
S9R+A15T+Q245F	N62D+I72V
S9R+A15T+Q245S	S9R+R19L+A98AD
S9R+A15T+T260M	S9G+P14R+R19I+A98AD
S9R+A15T	S9R+A15T+T22L+V139L+Q245V+A254S
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V139L+Q245F	S9R+A15T+Q245L
S9R+A15T+T22G+V139L+Q245L	S9R+A15T+N62NG+Q245T
S9R+A15T+Q245V	S9R+A15T+N62ND+V139L+Q245E
Q245F	S9R+A15T+N62ND+V139L+N261D
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S9R+A15T+G97GV+H120N	S9R+A15T+N62D+Q245W+N252S
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S9R+A15T+G97GV+H120E+Q137H	N218D+Q245W+N252E
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	Q245R
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S9R+A15T+G20*+L21F+N62E+Q245R	A98L+S99C+Q245R
V68A+S105G+S106A	V68A+S106A+T213A
S9R+A15T+Y167I+R170L	S9R+A15T+V68A
V68A+S106A+N252M+Y263C	V68A+S106A+Q245W
V68A+S106A+Q245R+N252D	V68A+S106A+Q245W+N252K
V68A+S106A+A174V+Q245R+N252D	S9R+A15T+V68A+Q245R+N252S
S9R+A15T+V28I+V68A+Q245R+N252A	S9R+A15T+V68A+A194T+Q245R+N252E
S9R+A15T+G20*+L21F+*63aG+Q245R+N272V	S9R+A15T+G20*+L21F+*62aS+N218D+Q245R
S9R+A15T+G20*+L21F+*61aS+V68A+G160D+Q245R	S9R+A15T+V68A+H120N+P131S+Q137H+Q245M



wherein

(a) the variant has protease activity, and

(b) each position corresponds to a position of the amino acid sequence of subtilisin BPN', shown in SEQ ID NO: 1.

5

4. The protease variant of claim 1, wherein the parent subtilase belongs to the sub-group I-S1.

10 5. The protease variant of claim 1, wherein the parent subtilase belongs to the sub-group I-S2, and wherein the parent subtilase preferably is subtilisin 309.

6. The protease variant of claim 1, wherein said variant further comprises one or more of the modifications K27R, \*36D, S56P, N62D, V68A, N76D, S87N, G97N, S99SE, S101G, S103A, V104A, V104I, V104N, V104Y, S106A, H120D, H120N, N123S, G159D, Y167A, 15 R170S, R170L, A194P, N204D, V205I, Q206E, L217D, N218S, N218D, M222S, M222A, T224S, A232V, K235L, Q236H, Q245R, N248D, N252K, T274A, S101G+V104N, S87N+S101G+V104N, K27R+V104Y+N123S+T274A, N76D+S103A+V104I, S99D+S101R+S103A+V104I+G160S, S3T+V4I+S99D+S101R+S103A+V104I+G160S+V199M+V205I+L217D, S3T+V4I+S99D+S101R+S103A+V104I+G160S+A194P+V199M+V205I+L217D, 20 S3T+V4I+S99D+S101R+S103A+V104I+G160S+V205I and N76D+V104A.

7. The protease variant of claim 1, comprising the following substitutions:  
S101G+S103A+V104I+G159D+A232V+Q236H+Q245R+N248D+N252K.

25 8. A cleaning or detergent composition, preferably a laundry or dish wash composition, comprising a protease variant of claim 1 and a surfactant.

9. A composition of claim 8, which additionally comprises one or more of an amylase, cellulase, cutinase, esterase, beta-galactosidase, glycoamylase, hemicellulase, lactase, 30 ligninase, lipase, polygalacturonase, and protease.

10. An isolated DNA sequence encoding a protease variant of claim 1

11. An expression vector comprising the isolated DNA sequence of claim 10.

12. A microbial host cell transformed with the expression vector of claim 11.
13. A microbial host cell of claim 12, which is a bacterium, preferably a *Bacillus*, especially a  
5 *B. lentus*.
14. A microbial host cell of claim 12, which is a fungus or yeast, preferably a filamentous  
fungus, especially an *Aspergillus*.
- 10 15. A method for producing a protease variant, comprising
- (a) culturing a host of claim 12 under conditions conducive to the expression and  
secretion of the variant, and
  - (b) recovering the protease variant.